



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: WILLIAMS, Lewis T.  
ESCOBEDO, Jaime A.
- (ii) TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Townsend and Townsend and Crew
  - (B) STREET: One Market, Steuart Street Tower, 20th Floor
  - (C) CITY: San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94105
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/461,917
  - (B) FILING DATE: 05-JUN-1995
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/309,322
  - (B) FILING DATE: 10-FEB-1989
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/151,414
  - (B) FILING DATE: 02-FEB-1988
- (ix) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Dow, Karen B.
  - (B) REGISTRATION NUMBER: 29,684
  - (C) REFERENCE/DOCKET NUMBER: 2307K-267-2-4
- (x) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 415/326-2400
  - (B) TELEFAX: 415/326-2422

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6373 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 129..3398
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGAGCTAC	AGGGAGAGAA	ACAGAGGAGG	AGACTGCAAG	AGATCATTGG	AGGCCGTGGG	60
CACGCTCTT	ACTCCATGTG	TGGGACATTC	ATTGCGGAAT	AACATCGGAG	GAGAAGTTTC	120
CCAGAGCT	ATG GGG ACT TCC CAT CCG GCG TTC CTG GTC TTA GGC TGT CTT					170
	Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu					
1	5		10			
CTC ACA GGG CTG AGC CTA ATC CTC TGC CAG CTT TCA TTA CCC TCT ATC						218
Leu Thr Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile						
15	20	25		30		
CTT CCA AAT GAA AAT GAA AAG GTT GTG CAG CTG AAT TCA TCC TTT TCT						266
Leu Pro Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser						
35	40		45			
CTG AGA TGC TTT GGG GAG AGT GAA GTG AGC TGG CAG TAC CCC ATG TCT						314
Leu Arg Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser						
50	55		60			
GAA GAA GAG AGC TCC GAT GTG GAA ATC AGA AAT GAA GAA AAC AAC AGC						362
Glu Glu Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser						
65	70		75			
GGC CTT TTT GTG ACG GTC TTG GAA GTG AGC AGT GCC TCG GCG GCC CAC						410
Gly Leu Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His						
80	85	90				
ACA GGG TTG TAC ACT TGC TAT TAC AAC CAC ACT CAG ACA GAA GAG AAT						458
Thr Gly Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn						
95	100	105		110		
GAG CTT GAA GGC AGG CAC ATT TAC ATC TAT GTG CCA GAC CCA GAT GTA						506
Glu Leu Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val						
115	120		125			
GCC TTT GTA CCT CTA GGA ATG ACG GAT TAT TTA GTC ATC GTG GAG GAT						554
Ala Phe Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp						
130	135		140			
GAT GAT TCT GCC ATT ATA CCT TGT CGC ACA ACT GAT CCC GAG ACT CCT						602
Asp Asp Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro						
145	150		155			
GTA ACC TTA CAC AAC AGT GAG GGG GTG GTA CCT GCC TCC TAC GAC AGC						650
Val Thr Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser						
160	165		170			
AGA CAG GGC TTT AAT GGG ACC TTC ACT GTA GGG CCC TAT ATC TGT GAG						698
Arg Gln Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu						
175	180		185		190	
GCC ACC GTC AAA GGA AAG AAG TTC CAG ACC ATC CCA TTT AAT GTT TAT						746
Ala Thr Val Lys Gly Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr						
195	200		205			
GCT TTA AAA GCA ACA TCA GAG CTG GAT CTA GAA ATG GAA GCT CTT AAA						794 -
Ala Leu Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys						
210	215		220			
ACC GTG TAT AAG TCA GGG GAA ACG ATT GTG GTC ACC TGT GCT GTT TTT						842
Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe						
225	230		235			
AAC AAT GAG GTG GTT GAC CTT CAA TGG ACT TAC CCT GGA GAA GTG AAA						890
Asn Asn Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys						
240	245		250			

GGC AAA GGC ATC ACA ATG CTG GAA GAA ATC AAA GTC CCA TCC ATC AAA Gly Lys Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys 255 260 265 270	938
TTG GTG TAC ACT TTG ACG GTC CCC GAG GCC ACG GTG AAA GAC AGT GGA Leu Val Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly 275 280 285	986
GAT TAC GAA TGT GCT GCC CGC CAG GCT ACC AGG GAG GTC AAA GAA ATG Asp Tyr Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met 290 295 300	1034
AAG AAA GTC ACT ATT TCT GTC CAT GAG AAA GGT TTC ATT GAA ATC AAA Lys Lys Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys 305 310 315	1082
CCC ACC TTC AGC CAG TTG GAA GCT GTC AAC CTG CAT GAA GTC AAA CAT Pro Thr Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His 320 325 330	1130
TTT GTT GTA GAG GTG CGG GCC TAC CCA CCT CCC AGG ATA TCC TGG CTG Phe Val Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu 335 340 345 350	1178
AAA AAC AAT CTG ACT CTG ATT GAA AAT CTC ACT GAG ATC ACC ACT GAT Lys Asn Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp 355 360 365	1226
GTG GAA AAG ATT CAG GAA ATA AGG TAT CGA AGC AAA TTA AAG CTG ATC Val Glu Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile 370 375 380	1274
CGT GCT AAG GAA GAA GAC AGT GGC CAT TAT ACT ATT GTA GCT CAA AAT Arg Ala Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn 385 390 395	1322
GAA GAT GCT GTG AAG AGC TAT ACT TTT GAA CTG TTA ACT CAA GTT CCT Glu Asp Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro 400 405 410	1370
TCA TCC ATT CTG GAC TTG GTC GAT GAT CAC CAT GGC TCA ACT GGG GGA Ser Ser Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly 415 420 425 430	1418
CAG ACG GTG AGG TGC ACA GCT GAA GGC ACG CCG CTT CCT GAT ATT GAG Gln Thr Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu 435 440 445	1466
TGG ATG ATA TGC AAA GAT ATT AAG AAA TGT AAT AAT GAA ACT TCC TGG Trp Met Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp 450 455 460	1514
ACT ATT TTG GCC AAC AAT GTC TCA AAC ATC ATC ACG GAG ATC CAC TCC Thr Ile Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser 465 470 475	1562
CGA GAC AGG AGT ACC GTG GAG GGC CGT GTG ACT TTC GCC AAA GTG GAG Arg Asp Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu 480 485 490	1610
GAG ACC ATC GCC GTG CGA TGC CTG GCT AAG AAT CTC CTT GGA GCT GAG Glu Thr Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu 495 500 505 510	1658
AAC CGA GAG CTG AAG CTG GTG GCT CCC ACC CTG CGT TCT GAA CTC ACG Asn Arg Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr 515 520 525	1706

GTG GCT GCT GCA GTC CTG GTG CTG TTG GTG ATT GTG ATC ATC TCA CTT	1754
Val Ala Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu	
530 535 540	
ATT GTC CTG GTT GTC ATT TGG AAA CAG AAA CCG AGG TAT GAA ATT CGC	1802
Ile Val Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg	
545 550 555	
TGG AGG GTC ATT GAA TCA ATC AGC CCA GAT GGA CAT GAA TAT ATT TAT	1850
Trp Arg Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr	
560 565 570	
GTG GAC CCG ATG CAG CTG CCT TAT GAC TCA AGA TGG GAG TTT CCA AGA	1898
Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg	
575 580 585 590	
GAT GGA CTA GTG CTT GGT CGG GTC TTG GGG TCT GGA GCG TTT GGG AAG	1946
Asp Gly Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys	
595 600 605	
GTG GTT GAA GGA ACA GCC TAT GGA TTA AGC CGG TCC CAA CCT GTC ATG	1994
Val Val Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met	
610 615 620	
AAA GTT GCA GTG AAG ATG CTA AAA CCC ACG GCC AGA TCC AGT GAA AAA	2042
Lys Val Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys	
625 630 635	
CAA GCT CTC ATG TCT GAA CTG AAG ATA ATG ACT CAC CTG GGG CCA CAT	2090
Gln Ala Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His	
640 645 650	
TTG AAC ATT GTA AAC TTG CTG GGA GCC TGC ACC AAG TCA GGC CCC ATT	2138
Leu Asn Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile	
655 660 665 670	
TAC ATC ATC ACA GAG TAT TGC TTC TAT GGA GAT TTG GTC AAC TAT TTG	2186
Tyr Ile Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu	
675 680 685	
CAT AAG AAT AGG GAT AGC TTC CTG AGC CAC CAC CCA GAG AAG CCA AAG	2234
His Lys Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys	
690 695 700	
AAA GAG CTG GAT ATC TTT GGA TTG AAC CCT GCT GAT GAA AGC ACA CGG	2282
Lys Glu Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg	
705 710 715	
AGC TAT GTT ATT TTA TCT TTT GAA AAC AAT GGT GAC TAC ATG GAC ATG	2330
Ser Tyr Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met	
720 725 730	
AAG CAG GCT GAT ACT ACA CAG TAT GTC CCC ATG CTA GAA AGG AAA GAG	2378
Lys Gln Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu	
735 740 745 750	
GTT TCT AAA TAT TCC GAC ATC CAG AGA TCA CTC TAT GAT CGT CCA GCC	2426
Val Ser Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala	
755 760 765	
TCA TAT AAG AAG AAA TCT ATG TTA GAC TCA GAA GTC AAA AAC CTC CTT	2474
Ser Tyr Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu	
770 775 780	
TCA GAT GAT AAC TCA GAA GGC CTT ACT TTA TTG GAT TTG TTG AGC TTC	2522
Ser Asp Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Phe	
785 790 795	

ACC TAT CAA GTT GCC CGA GGA ATG GAG TTT TTG GCT TCA AAA AAT TGT Thr Tyr Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys 800 805 810	2570
GTC CAC CGT GAT CTG GCT CGC AAC GTT CTC CTG GCA CAA GGA AAA Val His Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys 815 820 825 830	2618
ATT GTG AAG ATC TGT GAC TTT GGC CTG GCC AGA GAC ATC ATG CAT GAT Ile Val Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp 835 840 845	2666
TCG AAC TAT GTG TCG AAA GGC AGT ACC TTT CTG CCC GTG AAG TGG ATG Ser Asn Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met 850 855 860	2714
GCT CCT GAG AGC ATC TTT GAC AAC CTC TAC ACC ACA CTG AGT GAT GTC Ala Pro Glu Ser Ile Phe Asp Asn Leu Tyr Thr Leu Ser Asp Val 865 870 875	2762
TGG TCT TAT GGC ATT CTG CTC TGG GAG ATC TTT TCC CTT GGT GGC ACC Trp Ser Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr 880 885 890	2810
CCT TAC CCC GGC ATG ATG GTG GAT TCT ACT TTC TAC AAT AAG ATC AAG Pro Tyr Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys 895 900 905 910	2858
AGT GGG TAC CGG ATG GCC AAG CCT GAC CAC GCT ACC AGT GAA GTC TAC Ser Gly Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr 915 920 925	2906
GAG ATC ATG GTG AAA TGC TGG AAC AGT GAG CCG GAG AAG AGA CCC TCC Glu Ile Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser 930 935 940	2954
TTT TAC CAC CTG AGT GAG ATT GTG GAG AAT CTG CTG CCT GGA CAA TAT Phe Tyr His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr 945 950 955	3002
AAA AAG AGT TAT GAA AAA ATT CAC CTG GAC TTC CTG AAG AGT GAC CAT Lys Lys Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His 960 965 970	3050
CCT GCT GTG GCA CGC ATG CGT GTG GAC TCA GAC AAT GCA TAC ATT GGT Pro Ala Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly 975 980 985 990	3098
GTC ACC TAC AAA AAC GAG GAA GAC AAG CTG AAG GAC TGG GAG GGT GGT Val Thr Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly 995 1000 1005	3146
CTG GAT GAG CAG AGA CTG AGC GCT GAC AGT GGC TAC ATC ATT CCT CTG Leu Asp Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu 1010 1015 1020	3194
CCT GAC ATT GAC CCT GTC CCT GAG GAG GAC CTG GGC AAG AGG AAC Pro Asp Ile Asp Pro Val Pro Glu Glu Asp Leu Gly Lys Arg Asn 1025 1030 1035	3242
AGA CAC AGC TCG CAG ACC TCT GAA GAG AGT GCC ATT GAG ACG GGT TCC Arg His Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser 1040 1045 1050	3290
AGC AGT TCC ACC TTC ATC AAG AGA GAG GAC GAG ACC ATT GAA GAC ATC Ser Ser Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile 1055 1060 1065 1070	3338

GAC ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA GAC CTG GTG GAA GAC Asp Met Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp 1075 1080 1085	3386
AGC TTC CTG TAA CTGGCGGATT CGAGGGGTTTC CTTCCACTTC TGGGGCCACC Ser Phe Leu * 1090	3438
TCTGGATCCC GTTCAGAAAA CCACTTTATT GCAATGCGGA GGTTGAGAGG AGGACTTGGT TGATGTTAA AGAGAAGTTC CCAGCCAAGG GCCTCGGGGA GCCTTCTAA ATATGAATGA	3498 3558
ATGGGATATT TTGAAATGAA CTTTGTCACT GTTGCCTCTT GCAATGCCTC AGTAGCATCT CAGTGGTGTG TGAAGTTGG AGATAGATGG ATAAGGGAAT AATAGGCCAC AGAAGGTGAA	3618 3678
CTTTCTGCTT CAAGGACATT GGTGAGAGTC CAACAGACAC AATTTATACT GCGACAGAAC TTCAGCATTG TAATTATGTA AATAACTCTA ACCACGGCTG TGTTTAGATT GTATTAACTA	3738 3798
TCTTCTTGG ACTTCTGAAG AGACCACTCA ATCCATCCAT GTACTTCCCT CTTGAAACCT GATGTCAGCT GCTGTTGAAC TTTTAAAGA AGTGCATGAA AAACCATTG TGACCTTAAA	3858 3918
AGGTACTGGT ACTATAGCAT TTTGCTATCT TTTTAGTGT TAAAGAGATA AAGAATAATA ATTAACCAAC CTTGTTAAT AGATTTGGGT CATTAGAAG CCTGACAACT CATTTCATA	3978 4038
TTGTAATCTA TGTTTATAAT ACTACTACTG TTATCAGTAA TGCTAAATGT GTAATAATGT AACATGATT CCCTCCACAC AAAGCACAAT TTAAAAACAA TCCTTACTAA GTAGGTGATG	4098 4158
AGTTGACAG TTTTGACAT TTATATTAAA TAACATGTT CTCTATAAAG TATGGTAATA GCTTAGTGA ATTAAATTAA GTTGAGCATA GAGAACAAAG TAAAAGTAGT GTTGTCCAGG	4218 4278
AAGTCAGAAT TTTAACTGT ACTGAATAGG TTCCCCAATC CATCGTATTA AAAAACAAATT AACTGCCCTC TGAAATAATG GGATTAGAAA CAAACAAAAC TCTTAAGTCC TAAAAGTTCT	4338 4398
CAATGTAGAG GCATAAACCT GTGCTGAACA TAACTCTCA TGTATATTAC CCAATGGAAA ATATAATGAT CAGCGAAAAA GACTGGATTT GCAGAAGTTT TTTTTTTT TCTTCTTGCC	4458 4518
TGATGAAAGC TTTGGCGACC CCAATATATG TATTTTTGA ATCTATGAAC CTGAAAAGGG TCACAAAGGA TGCCCAGACA TCAGCCTCCT TCTTCACCC CTTACCCCAA AGAGAAAGAG	4578 4638
TTTGAAACTC GAGACCATAA AGATATTCTT TAGTGGAGGC TGGAAGTGCA TTAGCCTGAT CCTCAGTTCT CAAATGTGTG TGGCAGCCAG GTAGACTAGT ACCTGGGTTT CCATCCTTGA	4698 4758
GATTCTGAAG TATGAAGTCT GAGGGAAACC AGAGTCTGTA TTTTCTAAA CTCCCTGGCT GTTCTGATCG GCCAGGTTTC GGAAACACTG ACTTAGGTTT CAGGAAGTTG CCATGGGAAA	4818 4878
CAAATAATTG GAACTTTGGA ACAGGGTTCT TAAGTTGGTG CGTCCTTCGG ATGATAAAATT TAGGAACCGA AGTCCAATCA CTGTAAATTA CGGTAGATCG ATCGTTAACG CTGGAATTAA	4938 4998
ATTGAAAGGT CAGAATCGAC TCCGACTCTT TCGATTCAA ACCAAAAGTG TCCAAAAGGT TTTCATTCT ACGATGAAGG GTGACATACC CCCTCTAACT TGAAAGGGC AGAGGGCAGA	5058 5118
AGAGCGGAGG GTGAGGTATG GGGCGGTTCC TTTCCGTACA TGTTTTAAT ACGTTAAGTC ACAAGGTTCA GAGACACATT GGTGAGTCA CAAAACCACC TTTTTGTAA AATTCAAAAT	5178 5238

GACTATTAAA	CTCCAATCTA	CCCTCCTACT	TAACAGTGTA	GATAGGTGTG	ACAGTTGTC	5298
CAACCACACC	CAAGTAACCG	TAAGAAACGT	TATGACGAAT	TAACGACTAT	GGTATACTTA	5358
CTTTGTACCC	GACACTAATG	ACGTTAGTGA	CACGATAGCC	GTCTACTACG	AAACCTTCTA	5418
CGTCTTCGTT	ATTATTCAT	GAACTGATGG	ATGACCACAT	TAGAGTTACG	TTCGGGGTTG	5478
AAAGAATAGG	TTGAAAAAGT	ATCATTACG	CTTCTGACTC	GGTCTAACCG	GTAAATTTT	5538
CTTTGGACT	GATCCAAGAC	ATCTCGGTTA	ATCTGAACCT	TATGCAAACA	CAAAGATCTT	5598
AGTGTGAGT	TCGTAAGACA	AATAGCGAGT	GAGAGGGAAC	ATGTCGGAAT	AAAACAACCA	5658
CGAAACGTA	AACTATAACG	ACACTCGGAA	CGTACTGTAG	TACTCCGGCC	TACTTGAAG	5718
AGTCAGGTCA	TCAAAGGTCA	GGATTGTTA	CGAGGGTGG	CTTAAACATA	TACTGACGTA	5778
AACACCCACA	CACACACAAA	AGTCGTTAA	GGTCTAAACA	AAGGAAAACC	GGAGGACGTT	5838
TCAGAGGTCT	TCTTTAAC	GGTTAGAAAG	GATGAAAGAT	AAAAATACTA	CTGTTAGTT	5898
CGGCCGGACT	CTTGTGATA	AAACACTGAAA	AATTTGCTAA	TCACTACAGG	AATTTACAC	5958
CAGACGGTTA	GACATGTTT	ACCAGGATAA	AAACACTTCT	CCCTGTATTC	TATTTACTA	6018
CAATATGTAG	TTATACATAT	ATACATAAAG	ATATATCTGA	ACCTCTTATG	ACGGTTTTGT	6078
AAATACTGTT	CGACATAGTG	ACGGAAGCAA	ATATAAAAAA	ATTGACACTA	TTAGGGGTGT	6138
CCGTGTAATT	GACAACGTGA	AAACTTACAG	GTTTAAATA	TAAAATCTTT	ATTATTTTC	6198
TTCTATGAA	TGTACAAGGG	TTTGTACC	ACACCACTTA	CACACTCTT	TTGATTGAAC	6258
TATCCCAGAT	GGTTATGTT	TACATAATGC	TTACGGGGAC	AAGTACAAAA	ACAAAATTT	6318
GCACATTTAC	TTCTAGAAAT	ATAAAGTTAT	TTACTATATA	TTAAATTTCC	TTAAG	6373

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Thr	Ser	His	Pro	Ala	Phe	Leu	Val	Leu	Gly	Cys	Leu	Leu	Thr
1					5				10					15	

Gly	Leu	Ser	Leu	Ile	Leu	Cys	Gln	Leu	Ser	Leu	Pro	Ser	Ile	Leu	Pro
					20				25				30		

Asn	Glu	Asn	Glu	Lys	Val	Val	Gln	Leu	Asn	Ser	Ser	Phe	Ser	Leu	Arg
					35			40				45			

Cys	Phe	Gly	Glu	Ser	Glu	Val	Ser	Trp	Gln	Tyr	Pro	Met	Ser	Glu	Glu
	50					55				60					

Glu	Ser	Ser	Asp	Val	Glu	Ile	Arg	Asn	Glu	Glu	Asn	Asn	Ser	Gly	L u
	65				70				75				80		

Phe	Val	Thr	Val	Leu	Glu	Val	Ser	Ser	Ala	Ser	Ala	Ala	His	Thr	Gly
						85			90				95		

Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu  
 100 105 110

Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe  
 115 120 125

Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp  
 130 135 140

Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr  
 145 150 155 160

Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln  
 165 170 175

Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr  
 180 185 190

Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu  
 195 200 205

Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val  
 210 215 220

Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn  
 225 230 235 240

Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys  
 245 250 255

Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val  
 260 265 270

Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr  
 275 280 285

Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys  
 290 295 300

Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr  
 305 310 315 320

Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val  
 325 330 335

Val Glu Val Arg Ala Tyr Pro Pro Arg Ile Ser Trp Leu Lys Asn  
 340 345 350

Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu  
 355 360 365

Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala  
 370 375 380

Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp  
 385 390 395 400

Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser  
 405 410 415

Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr  
 420 425 430

Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met  
 435 440 445

Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile  
 450 455 460  
 Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp  
 465 470 475 480  
 Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr  
 485 490 495  
 Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg  
 500 505 510  
 Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala  
 515 520 525  
 Ala Ala Val Leu Val Leu Leu Val Ile Val Ile Ile Ser Leu Ile Val  
 530 535 540  
 Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg  
 545 550 555 560  
 Val Ile Glu Ser Ile Ser Pro Asp Gly His Glu Tyr Ile Tyr Val Asp  
 565 570 575  
 Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly  
 580 585 590  
 Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val  
 595 600 605  
 Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val  
 610 615 620  
 Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala  
 625 630 635 640  
 Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn  
 645 650 655  
 Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile  
 660 665 670  
 Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys  
 675 680 685  
 Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu  
 690 695 700  
 Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr  
 705 710 715 720  
 Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln  
 725 730 735  
 Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser  
 740 745 750  
 Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr  
 755 760 765  
 Lys Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp  
 770 775 780  
 Asp Asn Ser Glu Gly Leu Thr Leu Leu Asp Leu Leu Ser Ph Thr Tyr  
 785 790 795 800

Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His  
 805 810 815  
 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val  
 820 825 830  
 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn  
 835 840 845  
 Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro  
 850 855 860  
 Glu Ser Ile Phe Asp Asn Leu Tyr Thr Leu Ser Asp Val Trp Ser  
 865 870 875 880  
 Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr  
 885 890 895  
 Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly  
 900 905 910  
 Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile  
 915 920 925  
 Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr  
 930 935 940  
 His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys  
 945 950 955 960  
 Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala  
 965 970 975  
 Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr  
 980 985 990  
 Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp  
 995 1000 1005  
 Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp  
 1010 1015 1020  
 Ile Asp Pro Val Pro Glu Glu Asp Leu Gly Lys Arg Asn Arg His  
 1025 1030 1035 1040  
 Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser  
 1045 1050 1055  
 Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met  
 1060 1065 1070  
 Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe  
 1075 1080 1085  
 Leu \*  
 1090

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5427 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 187..3507

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTTCTCCTG AGCCTTCAGG AGCCTGCACC AGTCCTGCCT GTCCTTCTAC TCAGCTGTTA	60
CCCACTCTGG GACCAGCAGT CTTCTGATA ACTGGGAGAG GGCAGTAAGG AGGACTTCCT	120
GGAGGGGGTG ACTGTCCAGA GCCTGGAAC GTGCCACAC CAGAAGCCAT CAGCAGCAAG	180
GACACC ATG CGG CTT CCG GGT GCG ATG CCA GCT CTG GCC CTC AAA GGC Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly	228
1095 1100	
GAG CTG CTG TTG CTG TCT CTC CTG TTA CTT CTG GAA CCA CAG ATC TCT Glu Leu Leu Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser	276
1105 1110 1115 1120	
CAG GGC CTG GTC GTC ACA CCC CCG GGG CCA GAG CTT GTC CTC AAT GTC Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val	324
1125 1130 1135	
TCC AGC ACC TTC GTT CTG ACC TGC TCG GGT TCA GCT CCG GTG GTG TGG Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp	372
1140 1145 1150	
GAA CGG ATG TCC CAG GAG CCC CCA CAG GAA ATG GCC AAG GCC CAG GAT Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp	420
1155 1160 1165	
GGC ACC TTC TCC AGC GTG CTC ACA CTG ACC AAC CTC ACT GGG CTA GAC Gly Thr Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp	468
1170 1175 1180	
ACG GGA GAA TAC TTT TGC ACC CAC AAT GAC TCC CGT GGA CTG GAG ACC Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr	516
1185 1190 1195 1200	
GAT GAG CGG AAA CGG CTC TAC ATC TTT GTG CCA GAT CCC ACC GTG GGC Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly	564
1205 1210 1215	
TTC CTC CCT AAT GAT GCC GAG GAA CTA TTC ATC TTT CTC ACG GAA ATA Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile	612
1220 1225 1230	
ACT GAG ATC ACC ATT CCA TGC CGA GTA ACA GAC CCA CAG CTG GTG GTG Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val	660
1235 1240 1245	
ACA CTG CAC GAG AAG AAA GGG GAC GTT GCA CTG CCT GTC CCC TAT GAT Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp	708
1250 1255 1260	
CAC CAA CGT GGC TTT TCT GGT ATC TTT GAG GAC AGA AGC TAC ATC TGC His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys	756
1265 1270 1275 1280	
AAA ACC ACC ATT GGG GAC AGG GAG GTG GAT TCT GAT GCC TAC TAT GTC Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val	804
1285 1290 1295	

TAC AGA CTC CAG GTG TCA TCC ATC AAC GTC TCT GTG AAC GCA GTG CAG Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln 1300 1305 1310	852
ACT GTG GTC CGC CAG GGT GAG AAC ATC ACC CTC ATG TGC ATT GTG ATC Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile 1315 1320 1325	900
GGG AAT GAT GTG GTC AAC TTC GAG TGG ACA TAC CCC CGC AAA GAA AGT Gly Asn Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser 1330 1335 1340	948
GGG CGG CTG GTG GAG CCG GTG ACT GAC TTC CTC TTG GAT ATG CCT TAC Gly Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr 1345 1350 1355 1360	996
CAC ATC CGC TCC ATC CTG CAC ATC CCC AGT GCC GAG TTA GAA GAC TCG His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser 1365 1370 1375	1044
GGG ACC TAC ACC TGC AAT GTG ACG GAG AGT GTG AAT GAC CAT CAG GAT Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp 1380 1385 1390	1092
GAA AAG GCC ATC AAC ATC ACC GTG GTT GAG AGC GGC TAC GTG CGG CTC Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu 1395 1400 1405	1140
CTG GGA GAG GTG GGC ACA CTA CAA TTT GCT GAG CTG CAT CGG AGC CGG Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg 1410 1415 1420	1188
ACA CTG CAG GTA GTG TTC GAG GCC TAC CCA CCG CCC ACT GTC CTG TGG Thr Leu Gln Val Val Phe Glu Ala Tyr Pro Pro Thr Val Leu Trp 1425 1430 1435 1440	1236
TTC AAA GAC AAC CGC ACC CTG GGC GAC TCC AGC GCT GGC GAA ATC GCC Phe Lys Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala 1445 1450 1455	1284
CTG TCC ACG CGC AAC GTG TCG GAG ACC CGG TAT GTG TCA GAG CTG ACA Leu Ser Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr 1460 1465 1470	1332
CTG GTT CGC GTG AAG GTG GCA GAG GCT GGC CAC TAC ACC ATG CGG GCC Leu Val Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala 1475 1480 1485	1380
TTC CAT GAG GAT GCT GAG GTC CAG CTC TCC TTC CAG CTA CAG ATC AAT Phe His Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn 1490 1495 1500	1428
GTC CCT GTC CGA GTG CTG GAG CTA AGT GAG AGC CAC CCT GAC AGT GGG Val Pro Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly 1505 1510 1515 1520	1476
GAA CAG ACA GTC CGC TGT CGT GGC CGG GGC ATG CCG CAG CCG AAC ATC Glu Gln Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile 1525 1530 1535	1524
ATC TGG TCT GCC TGC AGA GAC CTC AAA AGG TGT CCA CGT GAG CTG CCG Ile Trp Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro 1540 1545 1550	1572
CCC ACG CTG CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG GAG ACT Pro Thr Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr 1555 1560 1565	1620

AAC GTG ACG TAC TGG GAG GAG CAG GAG TTT GAG GTG GTG AGC ACA	1668
Asn Val Thr Tyr Trp Glu Glu Gln Glu Phe Glu Val Val Ser Thr	
1570 1575 1580	
CTG CGT CTG CAG CAC GTG GAT CGG CCA CTG TCG GTG CGC TGC ACG CTG	1716
Leu Arg Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu	
1585 1590 1595 1600	
CGC AAC GCT GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC	1764
Arg Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His	
1605 1610 1615	
TCC TTG CCC TTT AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG	1812
Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val	
1620 1625 1630	
GTG CTC ACC ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG	1860
Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys	
1635 1640 1645	
AAG CCA CGT TAC GAG ATC CGA TGG AAG GTG ATT GAG TCT GTG AGC TCT	1908
Lys Pro Arg Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser	
1650 1655 1660	
GAC GGC CAT GAG TAC ATC TAC GTG GAC CCC ATG CAG CTG CCC TAT GAC	1956
Asp Gly His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp	
1665 1670 1675 1680	
TCC ACG TGG GAG CTG CCG CGG GAC CAG CTT GTG CTG GGA CGC ACC CTC	2004
Ser Thr Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu	
1685 1690 1695	
GGC TCT GGG GCC TTT GGG CAG GTG GTG GAG GCC ACA GCT CAT GGT CTG	2052
Gly Ser Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu	
1700 1705 1710	
AGC CAT TCT CAG GCC ACG ATG AAA GTG GCC GTC AAG ATG CTT AAA TCC	2100
Ser His Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser	
1715 1720 1725	
ACA GCC CGC AGC AGT GAG AAG CAA GCC CTT ATG TCG GAG CTG AAG ATC	2148
Thr Ala Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile	
1730 1735 1740	
ATG AGT CAC CTT GGG CCC CAC CTG AAC GTG GTC AAC CTG TTG GGG GCC	2196
Met Ser His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala	
1745 1750 1755 1760	
TGC ACC AAA GGA GGA CCC ATC TAT ATC ATC ACT GAG TAC TGC CGC TAC	2244
Cys Thr Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr	
1765 1770 1775	
GGA GAC CTG GTG GAC TAC CTG CAC CGC AAC AAA CAC ACC TTC CTG CAG	2292
Gly Asp Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln	
1780 1785 1790	
CAC CAC TCC GAC AAG CGC CGC CCG CCC AGC GCG GAG CTC TAC AGC AAT	2340
His His Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn	
1795 1800 1805	
GCT CTG CCC GTT GGG CTC CCC CTG CCC AGC CAT GTG TCC TTG ACC GGG	2388
Ala Leu Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly	
1810 1815 1820	
GAG AGC GAC GGT GGC TAC ATG GAC ATG AGC AAG GAC GAG TCG GTG GAC	2436
Glu Ser Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp	
1825 1830 1835 1840	

TAT GTG CCC ATG CTG GAC ATG AAA GGA GAC GTC AAA TAT GCA GAC ATC Tyr Val Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile 1845 1850 1855	2484
GAG TCC TCC AAC TAC ATG GCC CCT TAC GAT AAC TAC GTT CCC TCT GCC Glu Ser Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala 1860 1865 1870	2532
CCT GAG AGG ACC TGC CGA GCA ACT TTG ATC AAC GAG TCT CCA GTG CTA Pro Glu Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu 1875 1880 1885	2580
AGC TAC ATG GAC CTC GTG GGC TTC AGC TAC CAG GTG GCC AAT GGC ATG Ser Tyr Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met 1890 1895 1900	2628
GAG TTT CTG GCC TCC AAG AAC TGC GTC CAC AGA GAC CTG GCG GCT AGG Glu Phe Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg 1905 1910 1915 1920	2676
AAC GTG CTC ATC TGT GAA GGC AAG CTG GTC AAG ATC TGT GAC TTT GGC Asn Val Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly 1925 1930 1935	2724
CTG GCT CGA GAC ATC ATG CGG GAC TCG AAT TAC ATC TCC AAA GGC AGC Leu Ala Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser 1940 1945 1950	2772
ACC TTT TTG CCT TTA AAG TGG ATG GCT CCG GAG AGC ATC TTC AAC AGC Thr Phe Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser 1955 1960 1965	2820
CTC TAC ACC ACC CTG AGC GAC GTG TGG TCC TTC GGG ATC CTG CTC TGG Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp 1970 1975 1980	2868
GAG ATC TTC ACC TTG GGT GGC ACC CCT TAC CCA GAG CTG CCC ATG AAC Glu Ile Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn 1985 1990 1995 2000	2916
GAG CAG TTC TAC AAT GCC ATC AAA CGG GGT TAC CGC ATG GCC CAG CCT Glu Gln Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro 2005 2010 2015	2964
GCC CAT GCC TCC GAC GAG ATC TAT GAG ATC ATG CAG AAG TGC TGG GAA Ala His Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu 2020 2025 2030	3012
GAG AAG TTT GAG ATT CGG CCC CCC TTC TCC CAG CTG GTG CTG CTT CTC Glu Lys Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu 2035 2040 2045	3060
GAG AGA CTG TTG GGC GAA GGT TAC AAA AAG AAG TAC CAG CAG GTG GAT Glu Arg Leu Leu Gly Glu Gly Tyr Lys Lys Tyr Gln Gln Val Asp 2050 2055 2060	3108
GAG GAG TTT CTG AGG AGT GAC CAC CCA GCC ATC CTT CGG TCC CAG GCC Glu Glu Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala 2065 2070 2075 2080	3156
CGC TTG CCT GGG TTC CAT GGC CTC CGA TCT CCC CTG GAC ACC AGC TCC Arg Leu Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser 2085 2090 2095	3204
GTC CTC TAT ACT GCC GTG CAG CCC AAT GAG GGT GAC AAC GAC TAT ATC Val Leu Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile 2100 2105 2110	3252

ATC CCC CTG CCT GAC CCC AAA CCT GAG GTT GCT GAC GAG GGC CCA CTG Ile Pro Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu 2115 2120 2125	3300
GAG GGT TCC CCC AGC CTA GCC AGC TCC ACC CTG AAT GAA GTC AAC ACC Glu Gly Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr 2130 2135 2140	3348
TCC TCA ACC ATC TCC TGT GAC AGC CCC CTG GAG CCC CAG GAC GAA CCA Ser Ser Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro 2145 2150 2155 2160	3396
GAG CCA GAG CCC CAG CTT GAG CTC CAG GTG GAG CCG GAG CCG GAG CTG Glu Pro Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu 2165 2170 2175	3444
GAA CAG TTG CCG GAT TCG GGG TGC CCT GCG CCT CGG GCG GAA GCA GAG Glu Gln Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu 2180 2185 2190	3492
GAT AGC TTC CTG TAG GGGGCTGGCC CCTACCTGC CCTGCCTGAA GCTCCCCCGC Asp Ser Phe Leu * 2195	3547
TGCCAGCACC CAGCATCTCC TGGCCTGGCC TGGCCGGGCT TCCTGTCAGC CAGGCTGCC TTATCAGCTG TCCCCTCTG GAAGCTTCT GCTCCTGACG TGTTGTGCC CAAACCTGG GGCTGGCTTA GGAGGCAAGA AAAC TGCAAGG GGCGTGACCC AGCCCTCTGC CTCCAGGGAG GCCAACTGAC TCTGAGCCAG GGTTCCCCCA GGGAACTCAG TTTTCCATA TGTAAGATGG GAAAGTTAGG CTTGATGACC CAGAATCTAG GATTCTCTCC CTGGCTGACA GGTGGGGAGA CCGAATCCCT CCCTGGGAAG ATTCTTGGAG TTACTGAGGT GGTAAATTAA CTTTTTCTG TTCAGCCAGC TACCCCTCAA GGAATCATAG CTCTCTCCTC GCACTTTAT CCACCCAGGA GCTAGGGAAG AGACCCTAGC CTCCCTGGCT GCTGGCTGAG CTAGGGCCTA GCCTTGAGCA GTGTTGCCTC ATCCAGAAGA AAGCCAGTCT CCTCCCTATG ATGCCAGTCC CTGCGTTCCC TGGCCCGAGC TGGTCTGGGG CCATTAGGCA GCCTAATTAA TGCTGGAGGC TGAGCCAAGT ACAGGACACC CCCAGCCTGC AGCCCTTGCC CAGGGCACTT GGAGCACACG CAGCCATAGC AAGTGCCTGT GTCCCTGTCC TTCAGGCCCA TCAGTCCTGG GGCTTTTCT TTATCACCC CAGTCTTAAT CCATCCACCA GAGTCTAGAA GGCCAGACGG GCCCGCATC TGTGATGAGA ATGTAAATGT GCCAGTGTGG AGTGGCCACG TGTGTGTGCC AGATATGGCC CTGGCTCTGC ATTGGACCTG CTATGAGGCT TTGGAGGAAT CCCTCACCCCT CTCTGGGCCT CAGTTCCCC TTCAAAAAAT GAATAAGTCG GACTTATTAA CTCTGAGTGC CTTGCCAGCA CTAACATTCT AGAGTATCCA GGTGGTTGCA CATTGTCCA GATGAAGCAA GGCCATATAC CCTAAACTTC CATCCTGGGG GTCAGCTGGG CTCCTGGAG ATTCCAGATC ACACATCACA CTCTGGGGAC TCAGGAACCA TGCCCTTCC CCAGGCCCG AGCAAGTCTC AAGAACACAG CTGCACAGGC CTTGACTTAG AGTGACAGCC GGTGTCTGG AAAGCCCCA GCAGCTGCC CAGGGACATG GGAAGACCAC GGGACCTCTT TCACTACCCA CGATGACCTC CGGGGGTATC CTGGGCAAAA GGGACAAAGA GGGCAAATGA GATCACCTCC TGCAGCCAC CACTCCAGCA CCTGTGCCGA	3607 3667 3727 3787 3847 3907 3967 4027 4087 4147 4207 4267 4327 4387 4447 4507 4567 4627 4687 4747 4807 4867

GGTCTGCGTC GAAGACAGAA TGGACAGTGA GGACAGTTAT GTCTTGTAAA AGACAAGAAG	4927
CTTCAGATGG GTACCCCAAG AAGGATGTGA GAGGTGGCG CTTTGGAGGT TTGCCCTCA	4987
CCCACCAAGCT GCCCCATCCC TGAGGCAGCG CTCCATGGGG GTATGGTTT GTCACTGCC	5047
AGACCTAGCA GTGACATCTC ATTGTCCCCA GCCCAGTGGG CATTGGAGGT GCCAGGGAG	5107
TCAGGGTTGT AGCCAAGACG CCCCCGCACG GGGAGGGTTG GGAAGGGGT GCAGGAAGCT	5167
CAACCCCTCT GGGCACCAAC CCTGCATTGC AGGTTGGCAC CTTACTTCCC TGGGATCCCA	5227
GAGTTGGTCC AAGGAGGGAG AGTGGGTTCT CAATACGGTA CCAAAGATAT AATCACCTAG	5287
GTTTACAAAT ATTTTAGGA CTCACGTTAA CTCACATTTA TACAGCAGAA ATGCTATTTT	5347
GTATGCTGTT AAGTTTTCT ATCTGTGTAC TTTTTTTAA GGGAAAGATT TTAATATTAA	5407
ACCTGGTGCT TCTCACTCAC	5427

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu	
1 5 10 15	
Leu Leu Leu Ser Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly	
20 25 30	
Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser	
35 40 45	
Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg	
50 55 60	
Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr	
65 70 75 80	
Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly	
85 90 95	
Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu	
100 105 110	
Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu	
115 120 125	
Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu	
130 135 140	
Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu	
145 150 155 160	
His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln	
165 170 175	
Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr	
180 185 190	

Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg  
 195 200 205

Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val  
 210 215 220

Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn  
 225 230 235 240

Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg  
 245 250 255

Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile  
 260 265 270

Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr  
 275 280 285

Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys  
 290 295 300

Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly  
 305 310 315 320

Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu  
 325 330 335

Gln Val Val Phe Glu Ala Tyr Pro Pro Thr Val Leu Trp Phe Lys  
 340 345 350

Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser  
 355 360 365

Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr Leu Val  
 370 375 380

Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala Phe His  
 385 390 395 400

Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn Val Pro  
 405 410 415

Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly Glu Gln  
 420 425 430

Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile Ile Trp  
 435 440 445

Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro Pro Thr  
 450 455 460

Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val  
 465 470 475 480

Thr Tyr Trp Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg  
 485 490 495

Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn  
 500 505 510

Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu  
 515 520 525

Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu  
 530 535 540

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro  
 545 550 555 560  
 Arg Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly  
 565 570 575  
 His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr  
 580 585 590  
 Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser  
 595 600 605  
 Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His  
 610 615 620  
 Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala  
 625 630 635 640  
 Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser  
 645 650 655  
 His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr  
 660 665 670  
 Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp  
 675 680 685  
 Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln His His  
 690 695 700  
 Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu  
 705 710 715 720  
 Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser  
 725 730 735  
 Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val  
 740 745 750  
 Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser  
 755 760 765  
 Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu  
 770 775 780  
 Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr  
 785 790 795 800  
 Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe  
 805 810 815  
 Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val  
 820 825 830  
 Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala  
 835 840 845  
 Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe  
 850 855 860  
 Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr  
 865 870 875 880  
 Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile  
 885 890 895

Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu L u Pro Met Asn Glu Gln  
 900 905 910

Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His  
 915 920 925

Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys  
 930 935 940

Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg  
 945 950 955 960

Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp Glu Glu  
 965 970 975

Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu  
 980 985 990

Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu  
 995 1000 1005

Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro  
 1010 1015 1020

Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly  
 1025 1030 1035 1040

Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser  
 1045 1050 1055

Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro  
 1060 1065 1070

Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln  
 1075 1080 1085

Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser  
 1090 1095 1100

Phe Leu \*  
 1105

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro  
 1 5 10 15

Met Leu Asp Met  
 20

## (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719P. Contains a phosphate group at position 14."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro  
1 5 10 15

Met Leu Asp Met  
20

## (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708P. Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro  
1 5 10 15

Met Leu Asp Met  
20

## (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Peptide Y719P short."

Contains a phosphate group at position 11."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro Met Leu Asp  
1 5 10 15

Met

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..13
- (D) OTHER INFORMATION: /note= "Peptide Y708P short."

Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708P/F719."

Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Phe Val Pro  
1 5 10 15

Met Leu Asp Met  
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708/Y719P.

Contains a phosphate group at position 14."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly	Gly	Phe	Met	Asp	Met	Ser	Lys	Asp	Glu	Ser	Ile	Asp	Tyr	Val	Pro
1				5					10					15	
Met	Leu	Asp	Met												
			20												

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708P/Y719P.

Contains phosphate group at positions 3 & 14"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly	Gly	Tyr	Met	Asp	Met	Ser	Lys	Asp	Glu	Ser	Ile	Asp	Tyr	Val	Pro
1				5					10					15	
Met	Leu	Asp	Met												
			20												

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719P scrambled.

Contains a phosphate group at position 15."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Met	Asp	Ile	Lys	Val	Pro	Met	Asp	Glu	Tyr	Met	Ser	Asp	Tyr	Ser
1				5					10					15	

Asp Leu Gly Gly  
20

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURES:

- (D) OTHER INFORMATION: /note= "N is A, C, G, or T"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTSCGNGCN GCCAGNTCSC GNTG